



SEQUENCE LISTING

<10> The Government of the United States of America, as
represented by the Secretary, Department of Health and Human
Services, c/o Centers for Disease Control and Prevention
Chang, Gwong-Jen J.

<120> NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION

<130> 6395-64908

<150> PCT/US02/10764

<151> 2002-04-04

<150> 09/826,115

<151> 2001-04-04

<150> 09/701,536

<151> 2000-11-29

<150> PCT/US99/12298

<151> 1999-06-03

<150> 60/087,908

<151> 1998-06-04

<160> 61

<170> PatentIn version 3.2

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TECH CENTER 1600/2900

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 aagcatttat cagggttatt gtctcatgag cggatacata tttgaatgta ttagaaaaa 7449
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<210> 11
 <211> 697
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 11

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
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Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
 20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
 35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
 50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
 65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
 85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
 100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
 115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
 130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
 145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
 165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
 180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
 195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
 210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
 225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
 245 250 255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
 260 265 270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
 275 280 285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
 290 295 300

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
 305 310 315 320

Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
 325 330 335

Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
 340 345 350

Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
 355 360 365

Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
 370 375 380

Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
 385 390 395 400

Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
 405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
 420 425 430

Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
 435 440 445

Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
 450 455 460

Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
 465 470 475 480

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
 485 490 495

Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
 500 505 510

Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
 515 520 525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
 530 535 540

Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
 545 550 555 560

Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
 565 570 575

Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
 580 585 590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
 595 600 605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
 610 615 620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
 625 630 635 640

Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
 645 650 655

Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
 660 665 670

Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
 675 680 685

Val Phe Leu Ala Thr Asn Val His Ala
 690 695

<210> 12
 <211> 46
 <212> DNA
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<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> misc_feature
 <222> (1)..(46)
 <223> WN 466

<400> 12
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46

<210> 13
 <211> 43

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<212> DNA
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<220>
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<223> CWN2444

<400> 13
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<210> 14
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> MISC_FEATURE
<223> JE Signal

<400> 14

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1           5           10           15

Val Val Ile Ala Cys Ala Gly Ala
                20

<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (911)..(2986)

<400> 15
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ttagggtttag gcgtttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt	240
gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc	360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
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atcatatgcc aagtagccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca	600
tcgctattac catggtgatg cggtttttgg cagtacatca atgggcgtgg atagcggttt	660
gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac	720
caaatcaac gggactttcc aaaatgtcgt aacaactccg cccattgac gcaaatgggc	780
ggtaggcgtg tacgggtggga ggtctatata agcagagctc tctggctaac tagagaacct	840
actgcttact ggcttatcga aattaatacg actcactata gggagacca agcttggtac	900
cgccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg	949
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala	
1 5 10	
agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac	997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn	
15 20 25	
ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat	1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp	
30 35 40 45	
gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga	1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg	
50 55 60	
gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys	
65 70 75	
cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc	1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys	
80 85 90	
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
95 100 105	
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	

agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc	1333
Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
130 135 140	
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga	1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly	
145 150 155	
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc	1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
160 165 170	
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct	1477
Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala	
175 180 185	
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Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
190 195 200 205	
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc	1573
Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
210 215 220	
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg	1621
Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
225 230 235	
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg	1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
240 245 250	
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga	1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly	
255 260 265	
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa	1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln	
270 275 280 285	
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa	1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	
290 295 300	
gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata	1861
Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile	
305 310 315	
gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt	1909
Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe	
320 325 330	
gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag	1957
Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln	
335 340 345	
gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct	2005
Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro	
350 355 360 365	

tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt	2053
Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys	
370 375 380	
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt	2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val	
385 390 395	
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac	2149
Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn	
400 405 410	
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg	2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr	
415 420 425	
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca	2245
Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala	
430 435 440 445	
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att	2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile	
450 455 460	
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg	2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu	
465 470 475	
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat	2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr	
480 485 490	
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca	2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr	
495 500 505	
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga	2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly	
510 515 520 525	
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg	2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr	
530 535 540	
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg	2581
Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr	
545 550 555	
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca	2629
Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser	
560 565 570	
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac	2677
Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His	
575 580 585	
aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga	2725
Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly	
590 595 600 605	

gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser 610 615 620	2773
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gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln 640 645 650	2869
gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp 655 660 665	2917
agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe 670 675 680 685	2965
ctc tcc gtg aac gtg cac gcc tgaaggcggc cgctcgagca tgcacttaga Leu Ser Val Asn Val His Ala 690	3016
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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 16

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Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20           25           30

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Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
 35 40 45
 Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
 50 55 60
 Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
 65 70 75 80
 Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
 85 90 95
 Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
 100 105 110
 Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
 115 120 125
 Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
 130 135 140
 Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
 145 150 155 160
 Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
 165 170 175
 Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
 180 185 190
 Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
 195 200 205
 Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
 210 215 220
 Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
 225 230 235 240
 Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
 245 250 255
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
 260 265 270

Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
 275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300

Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
 305 310 315 320

Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335

Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
 340 345 350

Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
 355 360 365

Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
 370 375 380

Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
 385 390 395 400

Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
 405 410 415

Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
 420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
 435 440 445

Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
 450 455 460

Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
 465 470 475 480

Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
 485 490 495

Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
 500 505 510

Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
515 520 525

Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
530 535 540

Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
545 550 555 560

Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575

Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
580 585 590

Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
595 600 605

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
610 615 620

Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
660 665 670

Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
675 680 685

Asn Val His Ala
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<210> 17
<211> 5334
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature

<222> (1)..(5334)

<223> pCBE 1-14

<220>

<221> CDS

<222> (916)..(3006)

<400> 17

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
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atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
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tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc      900
tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
          Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
          1              5              10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
          15              20              25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
          30              35              40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
          45              50              55              60

gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
          65              70              75

gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
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Glu	Asp	Val	Asp	Cys	Trp	Cys	Asp	Asn	Gln	Glu	Val	Tyr	Val	Gln	Tyr	
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gga	cgg	tgc	acg	cgg	acc	agg	cat	tcc	aag	cga	agc	agg	aga	tcc	gtg	1287
Gly	Arg	Cys	Thr	Arg	Thr	Arg	His	Ser	Lys	Arg	Ser	Arg	Arg	Ser	Val	
	110					115					120					
tcg	gtc	caa	aca	cat	ggg	gag	agt	tca	cta	gtg	aat	aaa	aaa	gag	gct	1335
Ser	Val	Gln	Thr	His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala	
125					130					135					140	
tgg	ctg	gat	tca	acg	aaa	gcc	aca	cga	tat	ctc	atg	aaa	act	gag	aac	1383
Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	
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tgg	atc	ata	agg	aat	cct	ggc	tat	gct	ttc	ctg	gcg	gcg	gta	ctt	ggc	1431
Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	
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tgg	atg	ctt	ggc	agt	aac	aac	ggc	caa	cgc	gtg	gta	ttt	acc	atc	ctc	1479
Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	
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ctg	ctg	ttg	gtc	gct	ccg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527
Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	
	190					195					200					
aat	cgt	gac	ttc	ata	gaa	gga	gcc	agt	gga	gcc	act	tgg	gtg	gac	ttg	1575
Asn	Arg	Asp	Phe	Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	
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gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623
Val	Leu	Glu	Gly	Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	
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aca	ttg	gac	gtc	cgc	atg	att	aac	atc	gaa	gct	agc	caa	ctt	gct	gag	1671
Thr	Leu	Asp	Val	Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	
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gtc	aga	agt	tac	tgc	tat	cat	gct	tca	gtc	act	gac	atc	tcg	acg	gtg	1719
Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	
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gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767
Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	
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agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815
Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	
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gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863
Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	
				305					310					315		
tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911
Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	

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aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn 335 340 345			1959
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360			2007
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr 365 370 375 380			2055
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu 385 390 395			2103
gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg 400 405 410			2151
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gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala 430 435 440			2247
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His 445 450 455 460			2295
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tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala 480 485 490			2391
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495 500 505			2439
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510 515 520			2487
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525 530 535 540			2535
agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545 550 555			2583
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu 560 565 570			2631

560	565	570	
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gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635			2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650			2871
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met 655 660 665			2919
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<210> 18

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 18

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20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val

225		230		235		240
Arg Met Ile Asn	Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr					
	245		250		255	
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro						
	260		265		270	
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val						
	275		280		285	
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu						
	290		295		300	
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser						
305		310		315		320
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val						
	325		330		335	
Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr						
	340		345		350	
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro						
	355		360		365	
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr						
	370		375		380	
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val						
385		390		395		400
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His						
	405		410		415	
Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn						
	420		425		430	
Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser						
	435		440		445	
Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala						
	450		455		460	
Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly						

465		470		475		480
His Leu Lys Cys	Arg Leu Lys Met Asp	Lys Leu Ala Leu Lys	Gly Thr			
	485	490	495			
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala						
	500	505	510			
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser						
	515	520	525			
Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp						
	530	535	540			
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr						
	545	550	555			560
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly						
	565	570	575			
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His						
	580	585	590			
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu						
	595	600	605			
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe						
	610	615	620			
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln						
	625	630	635			640
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile						
	645	650	655			
Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala						
	660	665	670			
Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu						
	675	680	685			
Val Phe Leu Ala Thr Asn Val His Ala						
	690	695				

<210> 19

<211> 5283
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 19

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
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tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
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gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
      Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
      1          5          10

ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac      999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp
15          20          25          30

agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc      1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser
      35          40          45

cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg      1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met
      50          55          60

gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac      1143

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Gln	Glu	Glu	Glu	Pro	Val	Asp	Val	Asp	Cys	Phe	Cys	Arg	Gly	Val	Asp		
		80				85					90						
agg	gtt	aag	tta	gag	tat	gga	cgc	tgt	gga	agg	caa	gct	gga	tct	agg	1239	
Arg	Val	Lys	Leu	Glu	Tyr	Gly	Arg	Cys	Gly	Arg	Gln	Ala	Gly	Ser	Arg		
		95			100					105					110		
ggg	aaa	agg	tct	gtg	gtc	att	cca	aca	cat	gca	caa	aaa	gac	atg	gtc	1287	
Gly	Lys	Arg	Ser	Val	Val	Ile	Pro	Thr	His	Ala	Gln	Lys	Asp	Met	Val		
			115						120					125			
ggg	cga	ggg	cat	gca	tgg	ctt	aaa	ggg	gac	aat	att	cga	gat	cat	gtc	1335	
Gly	Arg	Gly	His	Ala	Trp	Leu	Lys	Gly	Asp	Asn	Ile	Arg	Asp	His	Val		
			130					135					140				
acc	cga	gtc	gag	ggc	tgg	atg	tgg	aag	aac	aag	ctt	cta	act	gcc	gcc	1383	
Thr	Arg	Val	Glu	Gly	Trp	Met	Trp	Lys	Asn	Lys	Leu	Leu	Thr	Ala	Ala		
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att	gtg	gcc	ttg	gct	tgg	ctc	atg	gtt	gat	agt	tgg	atg	gcc	aga	gtg	1431	
Ile	Val	Ala	Leu	Ala	Trp	Leu	Met	Val	Asp	Ser	Trp	Met	Ala	Arg	Val		
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act	gtc	atc	ctc	ttg	gcg	ttg	agt	cta	ggg	cca	gtg	tac	gcc	acg	agg	1479	
Thr	Val	Ile	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Pro	Val	Tyr	Ala	Thr	Arg		
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Cys	Thr	His	Leu	Glu	Asn	Arg	Asp	Phe	Val	Thr	Gly	Thr	Gln	Gly	Thr		
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acc	aga	gtg	tcc	cta	gtt	ttg	gaa	ctt	gga	ggc	tgc	gtg	acc	atc	aca	1575	
Thr	Arg	Val	Ser	Leu	Val	Leu	Glu	Leu	Gly	Gly	Cys	Val	Thr	Ile	Thr		
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gct	gag	ggc	aag	cca	tcc	att	gat	gta	tgg	ctc	gaa	gac	att	ttt	cag	1623	
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gaa	agc	ccg	gct	gaa	acc	aga	gaa	tac	tgc	ctg	cac	gcc	aaa	ttg	acc	1671	
Glu	Ser	Pro	Ala	Glu	Thr	Arg	Glu	Tyr	Cys	Leu	His	Ala	Lys	Leu	Thr		
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aac	aca	aaa	gtg	gag	gct	cgc	tgt	cca	acc	act	gga	ccg	gcg	aca	ctt	1719	
Asn	Thr	Lys	Val	Glu	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Pro	Ala	Thr	Leu		
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ccg	gag	gag	cat	cag	gct	aat	atg	gtg	tgc	aag	aga	gac	caa	agc	gac	1767	
Pro	Glu	Glu	His	Gln	Ala	Asn	Met	Val	Cys	Lys	Arg	Asp	Gln	Ser	Asp		
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cgt	gga	tgg	gga	aac	cac	tgc	ggg	ttt	ttt	ggg	aag	ggc	agt	ata	gtg	1815	
Arg	Gly	Trp	Gly	Asn	His	Cys	Gly	Phe	Phe	Gly	Lys	Gly	Ser	Ile	Val		
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Ala Cys	Ala Lys	Phe Glu	Cys Glu	Glu Ala	Lys Lys	Ala Val	Gly His	
305			310			315		
gtc tat	gac tcc	aca aag	atc acg	tat gtt	gtc aag	gtt gag	ccc cac	1911
Val Tyr	Asp Ser	Thr Lys	Ile Thr	Tyr Val	Val Lys	Val Glu	Pro His	
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aca ggg	gat tac	ttg gct	gca aat	gag acc	aat tca	aac agg	aaa tca	1959
Thr Gly	Asp Tyr	Leu Ala	Ala Asn	Glu Thr	Asn Ser	Asn Arg	Lys Ser	
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gca cag	ttt acg	gtg gca	tcc gag	aaa gtg	atc ctg	cgg ctc	ggc gac	2007
Ala Gln	Phe Thr	Val Ala	Ser Glu	Lys Val	Ile Leu	Arg Leu	Gly Asp	
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tat gga	gat gtg	tgc ctg	acg tgt	aaa gtg	gca agt	ggg att	gat gtc	2055
Tyr Gly	Asp Val	Ser Leu	Thr Cys	Lys Val	Ala Ser	Gly Ile	Asp Val	
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gcc caa	act gtg	gtg atg	tca ctc	gac agc	agc aag	gac cac	ctg cct	2103
Ala Gln	Thr Val	Val Met	Ser Leu	Asp Ser	Ser Lys	Asp His	Leu Pro	
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tct gca	tgg caa	gtg cac	cgt gac	tgg ttt	gag gac	ttg gcg	ctg ccc	2151
Ser Ala	Trp Gln	Val His	Arg Asp	Trp Phe	Glu Asp	Leu Ala	Leu Pro	
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tgg aaa	cac aag	gac aac	caa gat	tgg aac	agt gtg	gag aaa	ctt gtg	2199
Trp Lys	His Lys	Asp Asn	Gln Asp	Trp Asn	Ser Val	Glu Lys	Leu Val	
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gaa ttt	gga cca	cca cat	gct gtg	aaa atg	gat gtt	ttc aat	ctg ggg	2247
Glu Phe	Gly Pro	Pro His	Ala Val	Lys Met	Asp Val	Phe Asn	Leu Gly	
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gac cag	acg gct	gtg ctg	ctc aaa	tca ctg	gca gga	gtt ccg	ctg gcc	2295
Asp Gln	Thr Ala	Val Leu	Leu Lys	Ser Leu	Ala Gly	Val Pro	Leu Ala	
	450			455		460		
agt gtg	gag ggc	cag aaa	tac cac	ctg aaa	agc ggc	cat gtt	act tgt	2343
Ser Val	Glu Gly	Gln Lys	Tyr His	Leu Lys	Ser Gly	His Val	Thr Cys	
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gat gtg	gga ctg	gaa aag	ctg aaa	ctg aaa	ggc aca	acc tac	tcc atg	2391
Asp Val	Gly Leu	Glu Lys	Leu Lys	Leu Lys	Gly Thr	Thr Tyr	Ser Met	
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tgt gac	aaa gca	aag ttc	aaa tgg	aag aga	gtt cct	gtg gac	agc ggc	2439
Cys Asp	Lys Ala	Lys Phe	Lys Trp	Lys Arg	Val Pro	Val Asp	Ser Gly	
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cat gac	aca gta	gtc atg	gag gta	tca tac	aca gga	agc gac	aag cca	2487
His Asp	Thr Val	Val Met	Glu Val	Ser Tyr	Thr Gly	Ser Asp	Lys Pro	
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tgt cgg	atc ccg	gtg cgg	gct gtg	gca cat	ggg gtc	cca gcg	gtt aat	2535
Cys Arg	Ile Pro	Val Arg	Ala Val	Ala His	Gly Val	Pro Ala	Val Asn	
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gta gcc	atg ctc	ata acc	ccc aat	cca acc	att gaa	aca aat	ggg ggc	2583

Val	Ala	Met	Leu	Ile	Thr	Pro	Asn	Pro	Thr	Ile	Glu	Thr	Asn	Gly	Gly		
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Trp	Leu	Gly	Leu	Asn	Ala	Arg	Asn	Pro	Thr	Met	Ser	Met	Thr	Phe	Leu		
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gct	gtg	ggg	gct	ttg	aca	ctg	atg	atg	aca	atg	gga	ggt	ggg	gca		2964	
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tccagttcga tgtaaccac tcgtgcaccc aactgatctt cagcatcttt tactttcacc	5064
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<223> Description of artificial sequence; note = synthetic construct

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Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser Gln Val
35 40 45

Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met Gly Glu
50 55 60

Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp Gln Glu
65 70 75 80

Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp Arg Val
85 90 95

Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg Gly Lys
100 105 110

Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val Gly Arg
115 120 125

Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val Thr Arg
130 135 140

Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala Ile Val
145 150 155 160

Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val Thr Val
165 170 175

Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg Cys Thr
180 185 190

His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr Thr Arg
195 200 205

Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr Ala Glu
210 215 220

Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln Glu Ser
 225 230 235 240

Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr Asn Thr
 245 250 255

Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu Pro Glu
 260 265 270

Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp Arg Gly
 275 280 285

Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val Ala Cys
 290 295 300

Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His Val Tyr
 305 310 315 320

Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His Thr Gly
 325 330 335

Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser Ala Gln
 340 345 350

Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp Tyr Gly
 355 360 365

Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val Ala Gln
 370 375 380

Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro Ser Ala
 385 390 395 400

Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro Trp Lys
 405 410 415

His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val Glu Phe
 420 425 430

Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly Asp Gln
 435 440 445

Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala Ser Val
 450 455 460

Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys Asp Val
 465 470 475 480

Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met Cys Asp
 485 490 495

Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly His Asp
 500 505 510

Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro Cys Arg
 515 520 525

Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn Val Ala
 530 535 540

Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly Gly Phe
 545 550 555 560

Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Asp
 565 570 575

Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg Met Phe
 580 585 590

Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly Glu His
 595 600 605

Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val Gly Lys
 610 615 620

Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe Gly Gly
 625 630 635 640

Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val Trp Leu
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<210> 21
 <211> 5304
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<220>
<223> Description of artificial sequence; note = synthetic construct

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
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gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggac tatttacggg aaactgcccc cttggcagta catcaagtgt      480
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aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
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ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc      900
gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
      Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
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ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat      999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
15             20             25             30

cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc      1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
35             40             45

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct      1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
50             55             60

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca      1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
65             70             75

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Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp	
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Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His	
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tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc	1287
Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser	
115 120 125	
aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc	1335
Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr	
130 135 140	
aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat	1383
Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr	
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gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca	1431
Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr	
160 165 170	
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Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr	
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Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala	
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Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val	
210 215 220	
aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag	1623
Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys	
225 230 235	
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Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly	
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cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile 335 340 345 350	1959
gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser 355 360 365	2007
ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu 370 375 380	2055
gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys 385 390 395	2103
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu 400 405 410	2151
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu 415 420 425 430	2199
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu 435 440 445	2247
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro 450 455 460	2295
gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa Ala Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys 465 470 475	2343
tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly 480 485 490	2391
atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly 495 500 505 510	2439
cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro 515 520 525	2487
tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro 530 535 540	2535
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aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac	2631
Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr	
560 565 570	
atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa	2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys	
575 580 585 590	
gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc	2727
Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala	
595 600 605	
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Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile	
610 615 620	
gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga	2823
Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly	
625 630 635	
gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg	2871
Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly	
640 645 650	
cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg	2919
Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg	
655 660 665 670	
agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg	2967
Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu	
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Ala Thr Ser Val Gln Ala	
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aaactctcaa ggatcttacc gctgttgaga tccagttcga tgtaaccac tcgtgcaccc	5055
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caaatgccg caaaaaagg aataagggcg acacggaaat gttgaatact catactcttc	5175
ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg atacatattt	5235
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cctgacgtc	5304

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 <211> 692
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 22

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Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
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Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
35 40 45

Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
50 55 60

Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
85 90 95

Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100 105 110

Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115 120 125

Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145 150 155 160

Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
165 170 175

Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
180 185 190

Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
195 200 205

Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
210 215 220

Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
 225 230 235 240

Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
 245 250 255

Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
 260 265 270

Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
 275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300

Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
 305 310 315 320

Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335

Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
 340 345 350

Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
 355 360 365

Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
 370 375 380

Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
 385 390 395 400

Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
 405 410 415

Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
 420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
 435 440 445

Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
 450 455 460

Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
 465 470 475 480

Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
 485 490 495

Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
 500 505 510

Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
 515 520 525

Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
 530 535 540

Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
 545 550 555 560

Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
 565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
 580 585 590

Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
 595 600 605

Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
 610 615 620

Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
 625 630 635 640

Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
 645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
 660 665 670

Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
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Ser Val Gln Ala
 690

<210> 23
 <211> 5271
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
 ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
 gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata 300
 tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600
 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
 actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc 720
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg 780
 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc 900
 gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10
 ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
 15 20 25 30
 aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047
 Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr
 35 40 45
 ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag 1095
 Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys
 50 55 60

tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca	1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro	
65 70 75	
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac	1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn	
80 85 90	
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg	1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg	
95 100 105 110	
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag	1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys	
115 120 125	
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc	1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu	
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Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr	
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gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc	1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val	
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gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac	1479
Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His	
175 180 185 190	
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga	1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly	
195 200 205	
act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg	1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met	
210 215 220	
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att	1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile	
225 230 235	
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act	1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr	
240 245 250	
cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta	1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu	
255 260 265 270	
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Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp	
275 280 285	
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg	1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val	
290 295 300	

gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val 305 310 315	1863
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly 320 325 330	1911
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp 335 340 345 350	1959
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala 355 360 365	2007
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr 370 375 380	2055
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act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr 450 455 460	2295
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gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro 530 535 540	2535

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acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp 595 600 605	2727
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aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val 655 660 665 670	2919
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gcgagacca	cgctcaccgg	ctccagattt	atcagcaata	aaccagccag	ccggaagggc	4472
cgagcgcaga	agtggtcctg	caactttatc	cgctccatc	cagtctatta	attgttgccg	4532
ggaagctaga	gtaagtagtt	cgccagttaa	tagtttgccg	aacgttggtg	ccattgctac	4592
aggcatcgtg	gtgtcacgct	cgtcgttttg	tatggcttca	ttcagctccg	gttcccaacg	4652
atcaaggcga	gttacatgat	cccccatggt	gtgcaaaaaa	gcggttagct	ccttcgggtcc	4712
tccgatcgtt	gtcagaagta	agttggccgc	agtgttatca	ctcatgggta	tggcagcact	4772
gcataattct	cttactgtca	tgccatccgt	aagatgcttt	tctgtgactg	gtgagtactc	4832
aaccaagtca	ttctgagaat	agtgtatgcg	gcgaccgagt	tgctcttgcc	cggcgtcaat	4892
acgggataat	accgcgccac	atagcagaac	tttaaaagtg	ctcatcattg	gaaaacgttc	4952
ttcggggcga	aaactctcaa	ggatcttacc	gctgttgaga	tccagttcga	tgtaaccac	5012
tcgtgcaccc	aactgatctt	cagcatcttt	tactttcacc	agcgtttctg	ggtgagcaaa	5072
aacaggaagg	caaatgccg	caaaaaagg	aataagggcg	acacggaaat	gttgaatact	5132
catactcttc	ctttttcaat	attattgaag	catttatcag	ggttattgtc	tcatgagcgg	5192
atacatat	gaatgtat	agaaaaataa	acaaatagg	gttccgcgca	catttccccg	5252
aaaagtgcc	cctgacgtc					5271

<210> 24
 <211> 681
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
20 25 30

Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
35 40 45

Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
50 55 60

Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65 70 75 80

Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
85 90 95

Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
100 105 110

Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
115 120 125

Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
130 135 140

Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145 150 155 160

Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
165 170 175

Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
180 185 190

Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
195 200 205

Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
210 215 220

Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
 225 230 235 240

Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
 245 250 255

Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
 260 265 270

Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
 275 280 285

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
 290 295 300

Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
 305 310 315 320

Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
 325 330 335

Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
 340 345 350

Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
 355 360 365

Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
 370 375 380

Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
 385 390 395 400

Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
 405 410 415

His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
 420 425 430

Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
 435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
 450 455 460

His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
465 470 475 480

Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
485 490 495

Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
500 505 510

Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
515 520 525

Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
530 535 540

Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545 550 555 560

Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
565 570 575

Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
580 585 590

Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
595 600 605

Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
610 615 620

Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625 630 635 640

Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
645 650 655

Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
660 665 670

Met Phe Leu Ser Leu Gly Val Gly Ala
675 680

<210> 25

<211> 35

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <222> (1)..(35)
 <223> POW 454

 <400> 25
 aaaagaaaaa gcgctaccac catccaccgg gacag 35

 <210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <222> (1)..(41)
 <223> CPOW 2417

 <400> 26
 actgttacc tcaaccccg actcgccggc gaaaaagaaa a 41

 <210> 27
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <223> Modified JE Signal

 <400> 27

 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

 Val Val Ile Ala Gly Thr Ser Ala
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 <210> 28
 <211> 36
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <222> (1)..(36)
 <223> YF 482

 <400> 28
 aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac 36

 <210> 29
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <222> (1)..(41)
 <223> CYF 2433

 <400> 29
 acagagatcc tcaaccccg c actcgccggc gaaaaagaaa a 41

 <210> 30
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <222> (1)..(41)
 <223> SLE 463

 <400> 30
 aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a 41

 <210> 31
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> misc_feature
 <222> (1)..(40)
 <223> CSLE 2477

 <400> 31
 accggttggtc gcacgttcgg actcgccggc gaaaaagaaa 40

 <210> 32
 <211> 39
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 32

 Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
 1 5 10 15

 Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
 20 25 30

 Leu Leu Ser Thr Tyr Gln Gly
 35

 <210> 33
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 33

 Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
 1 5 10 15

 Lys Leu Ser Asn Phe Gln Gly Lys
 20

 <210> 34
 <211> 30
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 34

 Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile

1	5	10	15
---	---	----	----

Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
20 25 30

<210> 35
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 35

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30

Leu Ser Asn Phe Gln Gly Lys
35

<210> 36
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 36

Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1 5 10 15

Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
20 25 30

Gly Lys

<210> 37
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 37

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
 20 25 30

Lys

<210> 38
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 38

Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
 1 5 10 15

Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
 20 25 30

Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
 35 40 45

<210> 39
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 39

Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
 1 5 10 15

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
 20 25 30

Thr Val Arg Lys Glu Arg Gly Asp
 35 40

<210> 40
 <211> 24
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 40

Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 41

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 42

<211> 5292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 42

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ccgcatagtt aagccagtat ctgctccctg cttgtgtggt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420

attgacgtca atgggtggag tattttacggt aaactgcccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggtttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg attttcaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg	780
gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt	1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	

aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	
175 180 185 190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca	1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	
195 200 205	
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg	1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	
210 215 220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca	1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	
225 230 235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	
240 245 250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg	2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe 415 420 425 430	2199
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln 435 440 445	2247
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met 450 455 460	2295
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg 465 470 475	2343
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly 480 485 490	2391
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510	2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525	2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540	2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555	2583
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gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln 575 580 585 590	2679
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gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile 610 615 620	2775
gga aag gct ctc cac caa gtc ttt gga gca atc tat gga gct gcc ttc Gly Lys Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe 625 630 635	2823
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ttg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta	2919
Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val	
655 660 665 670	
ttg gtg gga att gtg aca ctg tat ttg gga gtc atg gtg cag gcc	2964
Leu Val Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala	
675 680 685	
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 tgcaaaaaag cggtagctc cttcggctct cgcacgttg tcagaagtaa gttggccgca 4764
 gtgttatcac tcatgggtat ggcagcactg cataattctc ttactgtcat gccatccgta 4824
 agatgctttt ctgtgactgg tgagtactca accaagtcac tctgagaata gtgtatgcgg 4884
 cgaccgagtt gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact 4944
 ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa aactctcaag gatcttaccg 5004
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 actttcacca gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga 5124
 ataaggcgca cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc 5184
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<210> 43

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 43

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
 100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
 115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
 130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
 145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
 165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
 180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
 195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
 210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
 225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
 245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
 260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
 275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
 290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
 305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
 325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly
625 630 635 640

Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile
645 650 655

Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val
660 665 670

Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
675 680 685

<210> 44
<211> 5293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2964)

<400> 44
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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggag tatttacggt aaactgcca cttggcagta catcaagtgt 480

atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggtttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggacttttcca aaatgtcgtg acaactccgc cccattgacg caaatgggcg	780
gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt	1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	

175	180	185	190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca				1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	195	200	205	
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg				1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	210	215	220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca				1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	225	230	235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag				1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	240	245	250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc				1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	255	260	265	270
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg				1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	275	280	285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc				1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	290	295	300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa				1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	305	310	315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac				1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	320	325	330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag				1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	335	340	345	350
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca				2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	355	360	365	
ggg tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac				2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	370	375	380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg				2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	385	390	395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg				2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	400	405	410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc				2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe				

415	420	425	430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa				2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln				
	435	440	445	
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg				2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met				
	450	455	460	
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga				2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg				
	465	470	475	
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga				2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly				
	480	485	490	
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata				2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile				
	495	500	505	510
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct				2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro				
	515	520	525	
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att				2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile				
	530	535	540	
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa				2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu				
	545	550	555	
gca gaa cct cca ttc gga gac agc cac atc atc ata gga gta gag ccg				2631
Ala Glu Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro				
	560	565	570	
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa				2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln				
	575	580	585	590
atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt				2727
Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly				
	595	600	605	
gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata				2775
Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile				
	610	615	620	
gga aag gct ctc cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt				2823
Gly Lys Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe				
	625	630	635	
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc				2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu				
	640	645	650	
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta				2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu				

655	660	665	670	
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct				2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala				
	675	680	685	
taattagttt gggcgggcgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc				3024
taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg				3084
tttgccctc ccccgctgct tccttgacct tggaagggtgc cactcccact gtcctttcct				3144
aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg				3204
gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg				3264
cgggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg				3324
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caggaaccgt aaaaaggcgg cgttgctggc gtttttccat aggctccgcc cccctgacga				3564
gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata				3624
ccaggcggtt cccctggaa gctccctcgt gcgctctcct gttccgacct tgccgcttac				3684
cggatacctg tccgccttct tcccttcggg aagcgtggcg ctttctcata gctcacgctg				3744
taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc				3804
cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggttaag				3864
acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag cgaggtatgt				3924
aggcggtgct acagagttct tgaagtgggt gcctaactac ggctacacta gaagaacagt				3984
at ttgggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg gtagctcttg				4044
atccggcaaaa caaaccaccg ctggtagcgg tgggtttttt gtttgcaagc agcagattac				4104
gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacgggggt ctgacgtca				4164
gtggaacgaa aactcacgtt aagggtttt ggtcatgaga ttatcaaaaa ggatcttcac				4224
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ttgggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt				4344
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accatctggc cccagtgtg caatgatacc gcgagacca cgctcaccgg ctccagattt				4464
atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc				4524
cgctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccaggttaa				4584


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catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5244
acaaataggg gttccgcga catttccccg aaaagtgcc cctgacgtc 5293

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<210> 45

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 45

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1           5           10           15

```

```

Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
          20           25           30

```

```

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
          35           40           45

```

```

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
50           55           60

```

```

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65           70           75           80

```

```

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
          85           90           95

```

```

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg

```

100					105					110					
Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	Leu	Glu
		115					120					125			
Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	His	Val
	130					135					140				
Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	Met	Met
145						150					155				160
Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala
				165					170					175	
Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	Met	Arg
			180					185					190		
Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly
	195						200					205			
Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met
	210					215					220				
Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala
225						230					235				240
Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr
				245					250					255	
Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu
			260					265					270		
Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp
		275					280					285			
Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val
	290					295					300				
Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val
305						310					315				320
Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly
				325					330					335	
Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile

340		345		350
Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr	355	360		365
Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn	370	375		380
Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg	385	390		395
Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr	405	410		415
Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn	420	425		430
Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly	435	440		445
Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser	450	455		460
Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp	465	470		475
Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe	485	490		495
Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile	500	505		510
Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu	515	520		525
Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val	530	535		540
Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu	545	550		555
Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln	565	570		575
Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe				

580

585

590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
 595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
 610 615 620

Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
 625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
 645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
 660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
 675 680 685

<210> 46
 <211> 5293
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<220>
 <221> CDS
 <222> (910) .. (2964)

<400> 46
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 ccgcatagtt aagccagtat ctgctccctg cttgtgtggt ggaggtcgct gagtagtgcg 120
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
 ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
 gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata 300
 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca 600

tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg	660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg	780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc'	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt	1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc	1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc	1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	
175 180 185 190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca	1527

Met	Arg	Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser		
				195					200					205			
gga	gga	agc	tgg	gtt	gac	ata	gtc	tta	gaa	cat	ggg	agc	tgt	gtg	acg	1575	
Gly	Gly	Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr		
			210					215					220				
acg	atg	gca	aaa	aac	aaa	cca	aca	ttg	gat	ttt	gaa	ctg	ata	aaa	aca	1623	
Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr		
		225					230					235					
gaa	gcc	aaa	cag	cct	gcc	acc	cta	agg	aag	tac	tgt	ata	gag	gca	aag	1671	
Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys		
	240					245					250						
cta	acc	aac	aca	aca	aca	gaa	tct	cgc	tgc	cca	aca	caa	ggg	gaa	ccc	1719	
Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro		
255					260				265						270		
agc	cta	aat	gaa	gag	cag	gac	aaa	agg	ttc	gtc	tgc	aaa	cac	tcc	atg	1767	
Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met		
			275					280						285			
gta	gac	aga	gga	tgg	gga	aat	gga	tgt	gga	cta	ttt	gga	aag	gga	ggc	1815	
Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly		
			290				295						300				
att	gtg	acc	tgt	gct	atg	ttc	aga	tgc	aaa	aag	aac	atg	gaa	gga	aaa	1863	
Ile	Val	Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys		
		305					310					315					
gtt	gtg	caa	cca	gaa	aac	ttg	gaa	tac	acc	att	gtg	ata	aca	cct	cac	1911	
Val	Val	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His		
	320					325					330						
tca	ggg	gaa	gag	cat	gca	gtc	gga	aat	gac	aca	gga	aaa	cat	ggc	aag	1959	
Ser	Gly	Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys		
335					340				345						350		
gaa	atc	aaa	ata	aca	cca	cag	agt	tcc	atc	aca	gaa	gca	gaa	ttg	aca	2007	
Glu	Ile	Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr		
				355					360					365			
ggc	tat	ggc	act	gtc	aca	atg	gag	tgc	tct	cca	aga	acg	ggc	ctc	gac	2055	
Gly	Tyr	Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp		
			370					375					380				
ttc	aat	gag	atg	gtg	ttg	ttg	cag	atg	gaa	aat	aaa	gct	tgg	ctg	gtg	2103	
Phe	Asn	Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val		
		385					390					395					
cac	agg	caa	tgg	ttc	cta	gac	ctg	ccg	tta	cca	tgg	ttg	ccc	gga	gcg	2151	
His	Arg	Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala		
	400					405					410						
gac	aca	caa	ggg	tca	aat	tgg	ata	cag	aaa	gag	aca	ttg	gtc	act	ttc	2199	
Asp	Thr	Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe		
415					420				425						430		
aaa	aat	ccc	cat	gcg	aag	aaa	cag	gat	gtt	gtt	gtt	tta	gga	tcc	caa	2247	

Lys	Asn	Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln		
				435					440					445			
gaa	ggg	gcc	atg	cac	aca	gca	ctt	aca	ggg	gcc	aca	gaa	atc	caa	atg	2295	
Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met		
			450					455					460				
tca	tca	gga	aac	tta	ctc	ttc	aca	gga	cat	ctc	aag	tgc	agg	ctg	aga	2343	
Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg		
		465					470					475					
atg	gac	aag	cta	cag	ctc	aaa	gga	atg	tca	tac	tct	atg	tgc	aca	gga	2391	
Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly		
	480					485					490						
aag	ttt	aaa	gtt	gtg	aag	gaa	ata	gca	gaa	aca	caa	cat	gga	aca	ata	2439	
Lys	Phe	Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile		
495					500				505						510		
gtt	atc	aga	gtg	caa	tat	gaa	ggg	gac	ggc	tct	cca	tgc	aag	atc	cct	2487	
Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro		
				515					520					525			
ttt	gag	ata	atg	gat	ttg	gaa	aaa	aga	cat	gtc	tta	ggc	cgc	ctg	att	2535	
Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile		
			530					535					540				
aca	gtc	aac	cca	att	gtg	aca	gaa	aaa	gat	agc	cca	gtc	aac	ata	gaa	2583	
Thr	Val	Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu		
		545					550					555					
gca	gaa	cct	cca	ttc	gga	gac	agc	tac	atc	atc	ata	gga	gta	gag	ccg	2631	
Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro		
	560					565					570						
gga	caa	ctg	aag	ctc	aac	tgg	ttt	aag	aaa	gga	agc	acg	ctg	ggc	aag	2679	
Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Thr	Leu	Gly	Lys		
575					580					585					590		
gcc	ttt	tca	aca	act	ttg	aag	gga	gct	caa	aga	ctg	gca	gcg	ttg	ggc	2727	
Ala	Phe	Ser	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly		
				595					600					605			
gac	aca	gcc	tgg	gac	ttt	ggc	tct	att	gga	ggg	gtc	ttc	aac	tcc	ata	2775	
Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile		
			610					615					620				
gga	aaa	gcc	gtt	cac	caa	gtg	ttt	ggc	ggc	gcc	ttc	aga	aca	ctc	ttt	2823	
Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe		
		625					630					635					
ggg	gga	atg	tct	tgg	atc	aca	caa	ggg	cta	atg	ggc	gcc	cta	ctg	ctc	2871	
Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu		
	640					645					650						
tgg	atg	ggc	gtc	aac	gca	cga	gac	cga	tca	att	gct	ttg	gcc	ttc	tta	2919	
Trp	Met	Gly	Val	Asn	Ala	Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu		
655					660					665					670		
gcc	aca	ggg	ggc	gtg	ctc	gtg	ttc	tta	gcg	acc	aat	gtg	cat	gct		2964	

Ala	Thr	Gly	Gly	Val	Leu	Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala	
				675					680					685	
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ctagatcctt	ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaaac										4284
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tcgttcatcc	atagttgcct	gactccccgt	cgtgtagata	actacgatac	gggagggcct										4404
accatctggc	cccagtgtgt	caatgatacc	gcgagacca	cgctcaccgg	ctccagattt										4464
atcagcaata	aaccagccag	ccggaagggc	cgagcgcaga	agtggtcctg	caactttatc										4524
cgctccatc	cagtctatta	attgttgccg	ggaagctaga	gtaagtagtt	cgccagttaa										4584
tagtttgctc	aacgttggtg	ccattgctac	aggcatcgtg	gtgtcacgct	cgtcgtttgg										4644
tatggcttca	ttcagctccg	gttcccaacg	atcaaggcga	gttacatgat	cccccatggt										4704

gtgcaaaaaa gcggttagct ccttcggtcc tccgatcggt gtcagaagta agttggccgc 4764
 agtgttatca ctcatgggta tggcagcact gcataattct cttactgtca tgccatccgt 4824
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 aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5184
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<210> 47

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 47

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
 20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
 100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
 115 120 125
 Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
 130 135 140
 Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
 145 150 155 160
 Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
 165 170 175
 Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
 180 185 190
 Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
 195 200 205
 Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
 210 215 220
 Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
 225 230 235 240
 Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
 245 250 255
 Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
 260 265 270
 Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
 275 280 285
 Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
 290 295 300
 Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
 305 310 315 320
 Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
 325 330 335
 Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
 340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
 355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
 370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
 385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
 405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
 420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
 435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
 450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
 465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
 485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
 500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
 515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
 530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
 545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
 565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe
 580 585 590

Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
610 615 620

Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 48
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 48
tgtgcaggcg ccttcattt aaccacacgt aacg 34

<210> 49
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 49
tcgagcggcc gctcaactaa ttaggcctgc accatgactc 40

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 50
cttatcgaaa ttaatacgac tcactatagg 30

<210> 51
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 51
 atagattgct ccaaacactt ggtgg 25

<210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 52
 actccatagg aaaagccgtt cacc 24

<210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 53
 gcgagctcta gcatttaggt gacactatag 30

<210> 54
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 54
 ctccaccaag tgtttggtgg tgccttcaga aca 33

<210> 55
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 55

Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr
 1 5 10

<210> 56
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 56
 cttatcgaaa ttaatacgac tcactatagg 30

 <210> 57
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 57
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 <210> 58
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

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 <223> Description of artificial sequence; note = synthetic construct

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<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 61

Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala
1 5 10